#3

SEQUENCE LISTING

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<120> Mammalian Proteins; Related Reagents and Methods

<130> DX01052K1

<140> 10/009,445
<141> 2000-05-11

<150> PCT/US00/12998
<151> 2000-05-11

<150> 9911123.9 GB
<151> 1999-05-13

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Met Leu Cys Phe Trp Arg Thr Ser
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cac gta gca gta ctc ttg atc tgg ggg gtc ttc gcg gct gag tca agt 162
His Val Ala Val Leu Leu Ile Trp Gly Val Phe Ala Ala Glu Ser Ser
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tgt cct gat aag aat caa aca atg cag aac aat tca tca act atg aca 210
Cys Pro Asp Lys Asn Gln Thr Met Gln Asn Asn Ser Ser Thr Met Thr
25 30 35 40

gaa gtt aac act aca gtg ttt gta cag atg ggt aaa aag gct ctg ctc 258
Glu Val Asn Thr Thr Val Phe Val Gln Met Gly Lys Lys Ala Leu Leu
45 50 55

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Cys Cys Pro Ser Ile Ser Leu Thr Lys Val Ile Leu Ile Thr Trp Thr
            60                  65                  70

ata acc ctc aga gga cag cct tcc tgc ata ata tcc tac aaa gca gac      354
Ile Thr Leu Arg Gly Gln Pro Ser Cys Ile Ile Ser Tyr Lys Ala Asp
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aca agg gag acc cat gaa agc aac tgc tcg gac aga agc atc acc tgg      402
Thr Arg Glu Thr His Glu Ser Asn Cys Ser Asp Arg Ser Ile Thr Trp
    90                  95                  100

gcc tcc aca cct gac ctc gct cct gac ctt cag atc agt gca gtg gcc      450
Ala Ser Thr Pro Asp Leu Ala Pro Asp Leu Gln Ile Ser Ala Val Ala
105                 110                 115                 120

ctc cag cat gaa ggg cgt tac tca tgt gat ata gca gta cct gac ggg      498
Leu Gln His Glu Gly Arg Tyr Ser Cys Asp Ile Ala Val Pro Asp Gly
                125                 130                 135

aat ttc caa aac atc tat gac ctc caa gtg ctg gtg ccc cct gaa gta      546
Asn Phe Gln Asn Ile Tyr Asp Leu Gln Val Leu Val Pro Pro Glu Val
            140                 145                 150

acc cac ttt cca ggg gaa aat aga act gca gtt tgt gag gcg att gca      594
Thr His Phe Pro Gly Glu Asn Arg Thr Ala Val Cys Glu Ala Ile Ala
        155                 160                 165

ggc aaa cct gct gcg cag atc tct tgg acg cca gat ggg gat tgt gtc      642
Gly Lys Pro Ala Ala Gln Ile Ser Trp Thr Pro Asp Gly Asp Cys Val
    170                 175                 180

gct aag aat gaa tca cac agc aat ggc acc gtg act gtc cgg agc aca      690
Ala Lys Asn Glu Ser His Ser Asn Gly Thr Val Thr Val Arg Ser Thr
185                 190                 195                 200

tgc cac tgg gag cag agc cac gtg tct gtc gtg ttc tgt gtt gtc tct      738
Cys His Trp Glu Gln Ser His Val Ser Val Val Phe Cys Val Val Ser
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cac ttg aca act ggt aac cag tct ctg tct ata gaa ctg ggt aga ggg      786
His Leu Thr Thr Gly Asn Gln Ser Leu Ser Ile Glu Leu Gly Arg Gly
            220                 225                 230

ggt gac caa tta tta gga tca tac att caa tac atc atc cca tct att      834
Gly Asp Gln Leu Leu Gly Ser Tyr Ile Gln Tyr Ile Ile Pro Ser Ile
        235                 240                 245

att att ttg atc atc ata gga tgc att tgt ctt ttg aaa atc agt ggc      882
Ile Ile Leu Ile Ile Ile Gly Cys Ile Cys Leu Leu Lys Ile Ser Gly
    250                 255                 260

tgc aga aaa tgt aaa ttg cca aaa tcg gga gct act cca gat att gag      930
Cys Arg Lys Cys Lys Leu Pro Lys Ser Gly Ala Thr Pro Asp Ile Glu
265                 270                 275                 280

gag gat gaa atg cag ccg tat gct agc tac aca gag aag agc aat cca      978
Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys Ser Asn Pro
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aaa gtc aat ggc aca gac tgt ctt act ttg tca gcc atg gga atc         1071
Lys Val Asn Gly Thr Asp Cys Leu Thr Leu Ser Ala Met Gly Ile
        315                 320                 325

tagaaccaag gaaaagaagt caagagacat cataattact gcttttcttt ctttaaactt   1131

ctccaatgga gggaaattag ctcttctgaa gttcttagaa agcacaaatg ttctaatgga   1191

tttgccttta agttcttcta tcattggaag tttggaatct ttgctgctac ctgttaattc   1251

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tatggtatgt gtgtgccttt atatgtttgt ttacaaatgt gtatatatgc acacatctga   1491

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        35                  40                  45

Gln Met Gly Lys Lys Ala Leu Leu Cys Cys Pro Ser Ile Ser Leu Thr
    50                  55                  60

Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser
65                  70                  75                  80

Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn
                85                  90                  95

Cys Ser Asp Arg Ser Ile Thr Trp Ala Ser Thr Pro Asp Leu Ala Pro
            100                 105                 110
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Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Arg Tyr Ser
115 120 125

Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu
130 135 140

Gln Val Leu Val Pro Pro Glu Val Thr His Phe Pro Gly Glu Asn Arg
145 150 155 160

Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser
165 170 175

Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn
180 185 190

Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val
195 200 205

Ser Val Val Phe Cys Val Val Ser His Leu Thr Thr Gly Asn Gln Ser
210 215 220

Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
225 230 235 240

Ile Gln Tyr Ile Ile Pro Ser Ile Ile Ile Leu Ile Ile Ile Gly Cys
245 250 255

Ile Cys Leu Leu Lys Ile Ser Gly Cys Arg Lys Cys Lys Leu Pro Lys
260 265 270

Ser Gly Ala Thr Pro Asp Ile Glu Glu Asp Glu Met Gln Pro Tyr Ala
275 280 285

Ser Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Thr Thr
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Thr Leu Ser Ala Met Gly Ile
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aagttgacca gagagggtct caccatgcgc acagttcctt ctgtaccagt gtggaggaaa 180

agtactgagt gaagggcaga aaaagagaaa acagaa atg ctc tgc cct tgg aga 234
Met Leu Cys Pro Trp Arg
1 5

act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc 282
Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu Thr Ile Phe Leu Val Ala
10 15 20

gaa gcg gag ggt gct gct caa cca aac aac tca tta atg ctg caa act 330
Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
25 30 35

agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa 378
Ser Lys Glu Asn His Ala Leu Ala Ser Ser Ser Leu Cys Met Asp Glu
40 45 50

aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act 426
Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
55 60 65 70

tca tgg cct gta aag atg gct aca aat gct gtg ctt tgt tgc cct cct 474
Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro
75 80 85

atc gca tta aga aat ttg atc ata ata aca tgg gaa ata atc ctg aga 522
Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg
90 95 100

ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca aat gag acc 570
Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr
105 110 115

aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct 618
Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro
120 125 130

gat cag aat tcg gac ctt cag att cgt acc gtg gcc atc act cat gac 666
Asp Gln Asn Ser Asp Leu Gln Ile Arg Thr Val Ala Ile Thr His Asp
135 140 145 150

ggg tat tac aga tgc ata atg gta aca cct gat ggg aat ttc cat cgt 714
Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg
155 160 165

gga tat cac ctc caa gtg tta gtt aca cct gaa gtg acc ctg ttt caa 762
Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln
170 175 180

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aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct      810
Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala
        185                 190                 195

gcg cat atc tcc tgg atc cca gag ggc gat tgt gcc act aag caa gaa      858
Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu
    200                 205                 210

tac tgg agc aat ggc aca gtg act gtt aag agt aca tgc cac tgg gag      906
Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu
215                 220                 225                 230

gtc cac aat gtg tct acc gtg acc tgc cac gtc tcc cat ttg act ggc      954
Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly
                235                 240                 245

aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa     1002
Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys
            250                 255                 260

atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta     1050
Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Tyr Leu
        265                 270                 275

gac cat cgt ggg att cat ttg gtt gtt gaa agt caa tgg ctg cag aaa     1098
Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys
    280                 285                 290

ata taaattgaat aaaacagaat ctactccagt tgttgaggag gatgaaatgc          1151
Ile
295

agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaaggtga   1211

aggcatctga ggcattacaa agtgaagttg acacagacct ccatacttta taagttgttg   1271

gactctagta ccaagaaaca acaacaaacg agatacatta taattactgt ctgattttct   1331

tacagttcta gaatgaagac ttatattgaa attaggtttt ccaaggttct tagaagacat   1391

tttaatggat tctcattcat acccttgtat aattggaatt tttgattctt agctgctacc   1451

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Ser Leu Met Leu Gln Thr Ser Lys Glu Asn His Ala Leu Ala Ser Ser
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Ser Leu Cys Met Asp Glu Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val
50 55 60

Leu Ala Glu Val Asn Thr Ser Trp Pro Val Lys Met Ala Thr Asn Ala
65 70 75 80

Val Leu Cys Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr
85 90 95

Trp Glu Ile Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys
100 105 110

Lys Glu Thr Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile
115 120 125

Thr Trp Val Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Thr
130 135 140

Val Ala Ile Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro
145 150 155 160

Asp Gly Asn Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro
165 170 175

Glu Val Thr Leu Phe Gln Asn Arg Asn Arg Thr Ala Val Cys Lys Ala
180 185 190

Val Ala Gly Lys Pro Ala Ala His Ile Ser Trp Ile Pro Glu Gly Asp
195 200 205

Cys Ala Thr Lys Gln Glu Tyr Trp Ser Asn Gly Thr Val Thr Val Lys
210 215 220

Ser Thr Cys His Trp Glu Val His Asn Val Ser Thr Val Thr Cys His
225 230 235 240

Val Ser His Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro
245 250 255

Val Pro Gly Ala Lys Lys Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His

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Pro Tyr Tyr Tyr Tyr Leu Asp His Arg Gly Ile His Leu Val Val Glu
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Ser Gln Trp Leu Gln Lys Ile
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Ile Trp Gly Val Phe Val Ala Gly Ser Ser Cys Thr Asp Lys Asn Gln
15                  20                  25                  30

aca aca cag aac aac agt tca tct cct ctg aca caa gtg aac act aca     147
Thr Thr Gln Asn Asn Ser Ser Ser Pro Leu Thr Gln Val Asn Thr Thr
                35                  40                  45

gtg tct gta cag ata ggt aca aag gct ctg ctc tgc tgc ttt tct att     195
Val Ser Val Gln Ile Gly Thr Lys Ala Leu Leu Cys Cys Phe Ser Ile
            50                  55                  60

cca ctg aca aaa gca gta tta atc aca tgg ata ata aag ctc aga ggc     243
Pro Leu Thr Lys Ala Val Leu Ile Thr Trp Ile Ile Lys Leu Arg Gly
        65                  70                  75

ctg cca tcc tgc aca ata gca tac aaa gta gat aca aag acc aat gaa     291
Leu Pro Ser Cys Thr Ile Ala Tyr Lys Val Asp Thr Lys Thr Asn Glu
    80                  85                  90

acc agc tgc ttg ggc agg aac atc acc tgg gcc tcc aca cct gac cac     339
Thr Ser Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro Asp His
95                  100                 105                 110

agt cct gaa ctt cag atc agt gca gtg acc ctc cag cat gag ggg act     387
Ser Pro Glu Leu Gln Ile Ser Ala Val Thr Leu Gln His Glu Gly Thr
                115                 120                 125

tac aca tgt gag aca gta aca cct gaa ggg aat ttt gaa aaa aac tat     435
Tyr Thr Cys Glu Thr Val Thr Pro Glu Gly Asn Phe Glu Lys Asn Tyr
            130                 135                 140

gac ctc caa gtg ctg gtg ccc cct gaa gta acc tac ttt cca gag aaa     483
Asp Leu Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Pro Glu Lys
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aac aga tct gca gtc tgt gag gca atg gca ggc aag cct gct gca cag      531
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    160                 165                 170

atc tct tgg tct cca gat ggg gac tgt gtc act acg agt gaa tca cac      579
Ile Ser Trp Ser Pro Asp Gly Asp Cys Val Thr Thr Ser Glu Ser His
175                 180                 185                 190

agc aat ggc act gtg act gtc agg agc aca tgc cac tgg gag cag aac      627
Ser Asn Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Asn
                195                 200                 205

aat gtg tct gat gtg tcc tgc att gtc tct cat ttg act ggt aac caa      675
Asn Val Ser Asp Val Ser Cys Ile Val Ser His Leu Thr Gly Asn Gln
            210                 215                 220

tct ctg tcc ata gaa ctg agt aga ggt ggt aac caa tca tta cga cca      723
Ser Leu Ser Ile Glu Leu Ser Arg Gly Gly Asn Gln Ser Leu Arg Pro
        225                 230                 235

tat att cca tac atc ata cca tca att atc att ttg atc atc ata gga      771
Tyr Ile Pro Tyr Ile Ile Pro Ser Ile Ile Ile Leu Ile Ile Ile Gly
    240                 245                 250

tgc att tgt ctt ttg aaa atc agt ggc ttc aga aaa tgc aaa ttg cca      819
Cys Ile Cys Leu Leu Lys Ile Ser Gly Phe Arg Lys Cys Lys Leu Pro
255                 260                 265                 270

aaa tta gaa gct act tca gct att gag gag gat gaa atg cag cct tat      867
Lys Leu Glu Ala Thr Ser Ala Ile Glu Glu Asp Glu Met Gln Pro Tyr
                275                 280                 285

gct agc tat aca gag aag agc aat cca ctc tat gat act gtg act aag      915
Ala Ser Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Lys
            290                 295                 300

gtg gag gca ttt cca gta tca caa ggc gaa gtc aat ggc aca gac tgc      963
Val Glu Ala Phe Pro Val Ser Gln Gly Glu Val Asn Gly Thr Asp Cys
        305                 310                 315

ctt act ttg tcg gcc att gga atc tagaaccaag aaaaaagaag tcaagagaca    1017
Leu Thr Leu Ser Ala Ile Gly Ile
    320                 325

tcataattac tgctttgctt tctttaaaat tcgacaatgg aaggactact tggaaattag   1077

ctcttccaaa gctattaaaa agcacaaatg ttctaatgaa attgcattta aattctatca   1137

ttggaagttt ggaatctctg ctgctacctg ttaattttag gaagaactga tttaattatt   1197

acaaagaaag cacatggtta tggtgaaata tcaagttgtg caataaagta tgatgaaaac   1257

tgagtttcct caagaaataa ctgcaggagg aacaatcatc actaaagaat ttcatgtgag   1317

ttcttacaaa aaaattccta tgtatacatg actatggtat gtgtgtccaa ttacatgttt   1377

atttacaaat gtgtatatat gcacacattt gcttttcagg acatctcctt gtaaaaaaca   1437

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Gln Asn Asn Ser Ser Ser Pro Leu Thr Gln Val Asn Thr Thr Val Ser
        35                  40                  45

Val Gln Ile Gly Thr Lys Ala Leu Leu Cys Cys Phe Ser Ile Pro Leu
    50                  55                  60

Thr Lys Ala Val Leu Ile Thr Trp Ile Ile Lys Leu Arg Gly Leu Pro
65                  70                  75                  80

Ser Cys Thr Ile Ala Tyr Lys Val Asp Thr Lys Thr Asn Glu Thr Ser
                85                  90                  95

Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro Asp His Ser Pro
            100                 105                 110

Glu Leu Gln Ile Ser Ala Val Thr Leu Gln His Glu Gly Thr Tyr Thr
        115                 120                 125

Cys Glu Thr Val Thr Pro Glu Gly Asn Phe Glu Lys Asn Tyr Asp Leu
    130                 135                 140

Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Pro Glu Lys Asn Arg
145                 150                 155                 160

Ser Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala Ala Gln Ile Ser
                165                 170                 175

Trp Ser Pro Asp Gly Asp Cys Val Thr Thr Ser Glu Ser His Ser Asn
            180                 185                 190

Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Asn Asn Val
        195                 200                 205
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Ser Asp Val Ser Cys Ile Val Ser His Leu Thr Gly Asn Gln Ser Leu
    210                 215                 220

Ser Ile Glu Leu Ser Arg Gly Gly Asn Gln Ser Leu Arg Pro Tyr Ile
225                 230                 235                 240

Pro Tyr Ile Ile Pro Ser Ile Ile Ile Leu Ile Ile Ile Gly Cys Ile
                245                 250                 255

Cys Leu Leu Lys Ile Ser Gly Phe Arg Lys Cys Lys Leu Pro Lys Leu
            260                 265                 270

Glu Ala Thr Ser Ala Ile Glu Glu Asp Glu Met Gln Pro Tyr Ala Ser
        275                 280                 285

Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Lys Val Glu
    290                 295                 300

Ala Phe Pro Val Ser Gln Gly Glu Val Asn Gly Thr Asp Cys Leu Thr
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Leu Ser Ala Ile Gly Ile
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1               5                   10                  15

ggt aac att tca cag cct gta ctg atg gat ata aat gct gtg ctt tgt      96
Gly Asn Ile Ser Gln Pro Val Leu Met Asp Ile Asn Ala Val Leu Cys
            20                  25                  30

tgc cct cct att gca tta aga aat ttg atc ata ata aca tgg gaa ata     144
Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile
        35                  40                  45

atc ctg aga ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca     192
Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr
    50                  55                  60

aat gag acc aag gaa acc aac tgt act gtt gag aga ata acc tgg gtc     240
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Asn Glu Thr Lys Glu Thr Asn Cys Thr Val Glu Arg Ile Thr Trp Val
65                  70                  75                  80

tct aga cct gat cag aat tcg gac ctt cag att cgt ccg gtg gac acc      288
Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Asp Thr
                85                  90                  95

act cat gac ggg tat tac aga ggc ata gtg gta aca cct gat ggg aat      336
Thr His Asp Gly Tyr Tyr Arg Gly Ile Val Val Thr Pro Asp Gly Asn
            100                 105                 110

ttc cat cgt gga tat cac ctc caa gtg tta gtt aca ccc gaa gtg aac      384
Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Asn
        115                 120                 125

cta ttt caa agc agg aat ata act gca gta tgc aag gca gtt aca ggg      432
Leu Phe Gln Ser Arg Asn Ile Thr Ala Val Cys Lys Ala Val Thr Gly
    130                 135                 140

aag cca gct gcc cag atc tcc tgg atc cca gag gga tct att ctt gcc      480
Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Ser Ile Leu Ala
145                 150                 155                 160

act aag caa gaa tac tgg ggc aat ggc aca gtg acg gtt aag agt aca      528
Thr Lys Gln Glu Tyr Trp Gly Asn Gly Thr Val Thr Val Lys Ser Thr
                165                 170                 175

tgc ccc tgg gag ggc cac aag tct act gtg acc tgc cat gtc tcc cat      576
Cys Pro Trp Glu Gly His Lys Ser Thr Val Thr Cys His Val Ser His
            180                 185                 190

ttg act ggc aac aag agt ctg tcc gta aag ttg aat tca ggt ctc aga      624
Leu Thr Gly Asn Lys Ser Leu Ser Val Lys Leu Asn Ser Gly Leu Arg
        195                 200                 205

acc tca gga tct cca gcg ttg tcc tta ctg atc att ctt tat gtg aaa      672
Thr Ser Gly Ser Pro Ala Leu Ser Leu Leu Ile Ile Leu Tyr Val Lys
    210                 215                 220

ctc tct ctt ttt gtg gtc att ctg gtc acc aca gga ttt gtt ttc ttc      720
Leu Ser Leu Phe Val Val Ile Leu Val Thr Thr Gly Phe Val Phe Phe
225                 230                 235                 240

cag agg ata aat cat gtc aga aaa gtt ctt taaagaagaa ggaagggtct        770
Gln Arg Ile Asn His Val Arg Lys Val Leu
                245                 250

tcttttgctt ctcctccttg tctctggact gcaacattgg tgagatgagt gatggtccag    830

cagtgaactt gggccatgga tgatgttaag gatagaagcc actcagtagg atagaagaaa    890

agaaagatgg aagaaggatc ctgggcttga tgaccatgaa gtttccctat aaaccctcaa    950

ccacctattc attgacttct tttgtgttag agtgaataaa attttgttca tgccagtgtt   1010
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<210> 8
<211> 250
<212> PRT
<213> Homo sapiens

<400> 8

Met Gly Gly Lys Gln Met Thr Gln Asn Tyr Ser Thr Ile Phe Ala Glu
1 5 10 15

Gly Asn Ile Ser Gln Pro Val Leu Met Asp Ile Asn Ala Val Leu Cys
20 25 30

Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile
35 40 45

Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr
50 55 60

Asn Glu Thr Lys Glu Thr Asn Cys Thr Val Glu Arg Ile Thr Trp Val
65 70 75 80

Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro Val Asp Thr
85 90 95

Thr His Asp Gly Tyr Tyr Arg Gly Ile Val Val Thr Pro Asp Gly Asn
100 105 110

Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Asn
115 120 125

Leu Phe Gln Ser Arg Asn Ile Thr Ala Val Cys Lys Ala Val Thr Gly
130 135 140

Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Ser Ile Leu Ala
145 150 155 160

Thr Lys Gln Glu Tyr Trp Gly Asn Gly Thr Val Thr Val Lys Ser Thr
165 170 175

Cys Pro Trp Glu Gly His Lys Ser Thr Val Thr Cys His Val Ser His
180 185 190

Leu Thr Gly Asn Lys Ser Leu Ser Val Lys Leu Asn Ser Gly Leu Arg
195 200 205

Thr Ser Gly Ser Pro Ala Leu Ser Leu Leu Ile Ile Leu Tyr Val Lys
210 215 220

Leu Ser Leu Phe Val Val Ile Leu Val Thr Thr Gly Phe Val Phe Phe
225 230 235 240

```
Gln Arg Ile Asn His Val Arg Lys Val Leu
                245                 250


<210>  9
<211>  1085
<212>  DNA
<213>  mus musculus

<220>
<221>  CDS
<222>  (1)..(582)
<223>


<400>  9
aga ggc cag cct tcc tgc ata atg gcc tac aaa gta gaa aca aag gag       48
Arg Gly Gln Pro Ser Cys Ile Met Ala Tyr Lys Val Glu Thr Lys Glu
1               5                   10                  15

acc aat gaa acc tgc ttg ggc agg aac atc acc tgg gcc tcc aca cct       96
Thr Asn Glu Thr Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro
            20                  25                  30

gac cac att cct gac ctt cag atc agt gcg gtg gcc ctc cag cat gag      144
Asp His Ile Pro Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu
        35                  40                  45

ggg aat tac tta tgt gag ata aca aca cct gaa ggg aat ttc cat aaa      192
Gly Asn Tyr Leu Cys Glu Ile Thr Thr Pro Glu Gly Asn Phe His Lys
    50                  55                  60

gtc tat gac ctc caa gtg ctg gtg ccc cct gaa gta acc tac ttt ctc      240
Val Tyr Asp Leu Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Leu
65                  70                  75                  80

ggg gaa aat aga act gca gtt tgt gag gca atg gca ggc aag cct gct      288
Gly Glu Asn Arg Thr Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala
                85                  90                  95

gca cag atc tct tgg act cca gat ggg gac tgt gtc act aag agt gag      336
Ala Gln Ile Ser Trp Thr Pro Asp Gly Asp Cys Val Thr Lys Ser Glu
            100                 105                 110

tca cac agc aat ggc act gtg act gtc agg agc act tgc cac tgg gag      384
Ser His Ser Asn Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu
        115                 120                 125

cag aac aat gtg tct gct gtg tcc tgc att gtc tct cat tcg act ggt      432
Gln Asn Asn Val Ser Ala Val Ser Cys Ile Val Ser His Ser Thr Gly
    130                 135                 140

aat cag tct ctg tcc ata gaa ctg agt aga ggt acc acc agc acc acc      480
Asn Gln Ser Leu Ser Ile Glu Leu Ser Arg Gly Thr Thr Ser Thr Thr
145                 150                 155                 160

cct tcc ttg ctg acc att ctc tac gtg aaa atg gtc ctt ttg ggg att      528
Pro Ser Leu Leu Thr Ile Leu Tyr Val Lys Met Val Leu Leu Gly Ile
                165                 170                 175
```

```
att ctt ctt aaa gtg gga ttt gct ttc ttc cag aag aga aat gtt acc      576
Ile Leu Leu Lys Val Gly Phe Ala Phe Phe Gln Lys Arg Asn Val Thr
            180                 185                 190

aga aca tgaatatcca gatttctgga agctcattag tctgatgaca cataccagaa      632
Arg Thr

aacagcattt gtaatcaact ttctcattgg aatccagctt acccgtccct gctgtcttca    692

tgtttgttag acactcacct ccaaattctt aactgagaag ggctcctgtc taaaggaaat    752

atggggacaa attgtggagc atagaccaaa agaaaggcca tccagagact gccccaccta    812

aggacccatc ccatatacag acaccaaacc cagacactac tgaagatgct gcgaagcgtt    872

tgctgacagg agcctgttat agctgtctcc tgagaggctc agccagagcc tgacaaatac    932

ataggtagat gcttgcagcc aacaactgga ctgagcaaaa aatctccatt ggaggagtta    992

gagaaaggac tgaagagggt gaaagggttt gcagccccat aggaagaaca acaatatcaa   1052

ccaaccagat ctcccagagc tcccagggac taa                               1085

<210>  10
<211>  194
<212>  PRT
<213>  mus musculus

<400>  10

Arg Gly Gln Pro Ser Cys Ile Met Ala Tyr Lys Val Glu Thr Lys Glu
1               5                   10                  15

Thr Asn Glu Thr Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro
            20                  25                  30

Asp His Ile Pro Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu
        35                  40                  45

Gly Asn Tyr Leu Cys Glu Ile Thr Thr Pro Glu Gly Asn Phe His Lys
    50                  55                  60

Val Tyr Asp Leu Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Leu
65                  70                  75                  80

Gly Glu Asn Arg Thr Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala
                85                  90                  95

Ala Gln Ile Ser Trp Thr Pro Asp Gly Asp Cys Val Thr Lys Ser Glu
            100                 105                 110

Ser His Ser Asn Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu
```

```
        115                 120                 125

Gln Asn Asn Val Ser Ala Val Ser Cys Ile Val Ser His Ser Thr Gly
    130                 135                 140

Asn Gln Ser Leu Ser Ile Glu Leu Ser Arg Gly Thr Thr Ser Thr Thr
145                 150                 155                 160

Pro Ser Leu Leu Thr Ile Leu Tyr Val Lys Met Val Leu Leu Gly Ile
                165                 170                 175

Ile Leu Leu Lys Val Gly Phe Ala Phe Phe Gln Lys Arg Asn Val Thr
            180                 185                 190

Arg Thr
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<210> 11
<211> 1354
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (42)..(875)
<223>

<400> 11

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ggcacgagtt acgatttgtg cttaacctga ctccactcca g atg cat gct ttg ggg     56
                                                  Met His Ala Leu Gly
                                                  1               5

agg act ctg gct ttg atg tta ctc atc ttc atc act att ttg gtg cct     104
Arg Thr Leu Ala Leu Met Leu Leu Ile Phe Ile Thr Ile Leu Val Pro
                10                  15                  20

gag tca agt tgt tca gtg aaa gga cgg gag gag atc cca ccg gat gat     152
Glu Ser Ser Cys Ser Val Lys Gly Arg Glu Glu Ile Pro Pro Asp Asp
            25                  30                  35

tca ttt cct ttt tca gat gat aat atc ttc cct gat gga gtg ggc gtc     200
Ser Phe Pro Phe Ser Asp Asp Asn Ile Phe Pro Asp Gly Val Gly Val
        40                  45                  50

acc atg gag att gag att atc act cca gtg tct gta cag ata ggt atc     248
Thr Met Glu Ile Glu Ile Ile Thr Pro Val Ser Val Gln Ile Gly Ile
    55                  60                  65

aag gct cag ctt ttc tgt cat cct agt cca tca aaa gaa gca aca ctt     296
Lys Ala Gln Leu Phe Cys His Pro Ser Pro Ser Lys Glu Ala Thr Leu
70                  75                  80                  85

aga ata tgg gaa ata act ccc aga gac tgg cct tcc tgc aga cta ccc     344
Arg Ile Trp Glu Ile Thr Pro Arg Asp Trp Pro Ser Cys Arg Leu Pro
```

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                    90                  95                  100

tac aga gca gag ttg cag cag atc agt aaa aaa atc tgt act gag aga      392
Tyr Arg Ala Glu Leu Gln Gln Ile Ser Lys Lys Ile Cys Thr Glu Arg
            105                 110                 115

gga acc act agg gtc cct gca cat cac cag agt tct gac ctt ccc atc      440
Gly Thr Thr Arg Val Pro Ala His His Gln Ser Ser Asp Leu Pro Ile
        120                 125                 130

aaa tca atg gcc ctc aag cat gat ggg cat tac tca tgt cgg ata gaa      488
Lys Ser Met Ala Leu Lys His Asp Gly His Tyr Ser Cys Arg Ile Glu
    135                 140                 145

aca aca gat ggg att ttc caa gag aga cat agc atc caa gtg cca ggg      536
Thr Thr Asp Gly Ile Phe Gln Glu Arg His Ser Ile Gln Val Pro Gly
150                 155                 160                 165

gaa aat aga act gta gtt tgt gag gca att gca agc aag cct gct atg      584
Glu Asn Arg Thr Val Val Cys Glu Ala Ile Ala Ser Lys Pro Ala Met
                170                 175                 180

cag atc ttg tgg act cca gat gag gac tgt gtc act aag agt aaa tca      632
Gln Ile Leu Trp Thr Pro Asp Glu Asp Cys Val Thr Lys Ser Lys Ser
            185                 190                 195

cac aat gac acc atg att gtc agg agc aag tgc cac agg gag aaa aac      680
His Asn Asp Thr Met Ile Val Arg Ser Lys Cys His Arg Glu Lys Asn
        200                 205                 210

aat ggc cac agt gtg ttc tgc ttt atc tcc cat ttg act gat aac tgg      728
Asn Gly His Ser Val Phe Cys Phe Ile Ser His Leu Thr Asp Asn Trp
    215                 220                 225

att ctc tcc atg gaa cag aat cga ggt aca acc agc atc ctg cct tcc      776
Ile Leu Ser Met Glu Gln Asn Arg Gly Thr Thr Ser Ile Leu Pro Ser
230                 235                 240                 245

ttg ctg agc att ctc tat gtg aaa ctg gct gta act gtt ctc atc gta      824
Leu Leu Ser Ile Leu Tyr Val Lys Leu Ala Val Thr Val Leu Ile Val
                250                 255                 260

gga ttt gct ttt ttc cag aag aga aat tat ttc aga gtg cca gaa ggc      872
Gly Phe Ala Phe Phe Gln Lys Arg Asn Tyr Phe Arg Val Pro Glu Gly
            265                 270                 275

tcc tgaggagagt ggtctgtggt taagatgaga tttaccacca tctgaaagac          925
Ser

atcttgtcta ccgcgcagcg tgctgagatt ccgagaagca gccacagaac ctactaggaa    985

gacaaatctg atgtggttgt caatcctttc aatggacctg agtacttcta taaacccgag   1045

tgaggttgtg ctggacccag gagccaggct aggtcatata tgttgatttt tgctgcaaga   1105

cctcatggtt tatctacaaa tcctaaattc tttcacttcc agttttaaaa cttttggccc   1165

aagcatttta tccacagcat aacaccttta aagaaactct cccacggaaa ctgctggttc   1225

catggaatgg aaaattgcaa catggtttac aagacagtgc aaaccaagca gcattccaag   1285
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atatgagctt cagaaagtta caggaactgt cttgggacga gaaagaagga ttaaatagtt 1345

cccagtccc 1354

<210> 12
<211> 278
<212> PRT
<213> Mus musculus

<400> 12

Met His Ala Leu Gly Arg Thr Leu Ala Leu Met Leu Leu Ile Phe Ile
1 5 10 15

Thr Ile Leu Val Pro Glu Ser Ser Cys Ser Val Lys Gly Arg Glu Glu
20 25 30

Ile Pro Pro Asp Asp Ser Phe Pro Phe Ser Asp Asp Asn Ile Phe Pro
35 40 45

Asp Gly Val Gly Val Thr Met Glu Ile Glu Ile Ile Thr Pro Val Ser
50 55 60

Val Gln Ile Gly Ile Lys Ala Gln Leu Phe Cys His Pro Ser Pro Ser
65 70 75 80

Lys Glu Ala Thr Leu Arg Ile Trp Glu Ile Thr Pro Arg Asp Trp Pro
85 90 95

Ser Cys Arg Leu Pro Tyr Arg Ala Glu Leu Gln Gln Ile Ser Lys Lys
100 105 110

Ile Cys Thr Glu Arg Gly Thr Thr Arg Val Pro Ala His His Gln Ser
115 120 125

Ser Asp Leu Pro Ile Lys Ser Met Ala Leu Lys His Asp Gly His Tyr
130 135 140

Ser Cys Arg Ile Glu Thr Thr Asp Gly Ile Phe Gln Glu Arg His Ser
145 150 155 160

Ile Gln Val Pro Gly Glu Asn Arg Thr Val Val Cys Glu Ala Ile Ala
165 170 175

Ser Lys Pro Ala Met Gln Ile Leu Trp Thr Pro Asp Glu Asp Cys Val
180 185 190

Thr Lys Ser Lys Ser His Asn Asp Thr Met Ile Val Arg Ser Lys Cys
195 200 205

His Arg Glu Lys Asn Asn Gly His Ser Val Phe Cys Phe Ile Ser His
210 215 220

Leu Thr Asp Asn Trp Ile Leu Ser Met Glu Gln Asn Arg Gly Thr Thr
225 230 235 240

Ser Ile Leu Pro Ser Leu Leu Ser Ile Leu Tyr Val Lys Leu Ala Val
245 250 255

Thr Val Leu Ile Val Gly Phe Ala Phe Phe Gln Lys Arg Asn Tyr Phe
260 265 270

Arg Val Pro Glu Gly Ser
275

<210> 13
<211> 981
<212> DNA
<213> rodent

<220>
<221> misc_feature
<222> (1)..(981)
<223> n may be a, c, g, or t.

<400> 13
atgytntgyt tytggmgnac nwsncaygtn gcngtnytny tnathtgggg ngtnttygcn 60

gcngarwsnw sntgyccnga yaaraaycar acnatgcara ayaaywsnws nacnatgacn 120

gargtnaaya cnacngtntt ygtncaratg ggnaaraarg cnytnytntg ytgyccnwsn 180

athwsnytna cnaargtnat hytnathacn tggacnatha cnytnmgngg ncarccnwsn 240

tgyathathw sntayaargc ngayacnmgn garacncayg arwsnaaytg ywsngaymgn 300

wsnathacnt gggcnwsnac nccngayytn gcnccngayy tncarathws ngcngtngcn 360

ytncarcayg arggnmgnta ywsntgygay athgcngtnc cngayggnaa yttycaraay 420

athtaygayy tncargtnyt ngtnccnccn gargtnacnc ayttyccngg ngaraaymgn 480

acngcngtnt gygargcnat hgcnggnaar ccngcngcnc arathwsntg gacnccngay 540

ggngaytgyg tngcnaaraa ygarwsncay wsnaayggna cngtnacngt nmgnwsnacn 600

tgycaytggg arcarwsnca ygtnwsngtn gtnttytgyg tngtnwsnca yytnacnacn 660

ggnaaycarw snytnwsnat hgarytnggn mgnggnggng aycarytnyt nggnwsntay 720

athcartaya thathccnws nathathath ytnathatha thggntgyat htgyytnytn 780

aarathwsng gntgymgnaa rtgyaarytn ccnaarwsng gngcnacncc ngayathgar 840

gargaygara tgcarccnta ygcnwsntay acngaraarw snaayccnyt ntaygayacn 900

gtnacnacna cngargcnca yccngcnwsn carggnaarg tnaayggnac ngaytgyytn 960

acnytnwsng cnatgggnat h 981

<210> 14
<211> 885
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(885)
<223> N may be a, c, g, or t.

<400> 14
atgytntgyc cntggmgnac ngcnaayytn ggnytnytny tnathytnac nathttyytn 60

gtngcngarg cngarggngc ngcncarccn aayaaywsny tnatgytnca racnwsnaar 120

garaaycayg cnytngcnws nwsnwsnytn tgyatggayg araarcarat hacncaraay 180

taywsnaarg tnytngcnga rgtnaayacn wsntggccng tnaaratggc nacnaaygcn 240

gtnytntgyt gyccnccnat hgcnytnmgn aayytnatha thathacntg ggarathath 300

ytnmgnggnc arccnwsntg yacnaargcn tayaaraarg aracnaayga racnaargar 360

acnaaytgya cngaygarmg nathacntgg gtnwsnmgnc cngaycaraa ywsngayytn 420

carathmgna cngtngcnat hacncaygay ggntaytaym gntgyathat ggtnacnccn 480

gayggnaayt tycaymgngg ntaycayytn cargtnytng tnacnccnga rgtnacnytn 540

ttycaraaym gnaaymgnac ngcngtntgy aargcngtng cnggnaarcc ngcngcncay 600

athwsntgga thccngargg ngaytgygcn acnaarcarg artaytggws naayggnacn 660

gtnacngtna arwsnacntg ycaytgggar gtncayaayg tnwsnacngt nacntgycay 720

gtnwsncayy tnacnggnaa yaarwsnytn tayathgary tnytnccngt nccnggngcn 780

aaraarathw snaarathat htaywsnath taycayccnt aytaytayta yytngaycay 840

mgnggnathc ayytngtngt ngarwsncar tggytncara arath 885

<210> 15
<211> 978
<212> DNA
<213> rodent

<220>
<221> misc_feature
<222> (1)..(978)

<223> n may be a, c, g, or t.

<400> 15
atgttytgyt tytggmgnac nwsngcnytn gcngtnytny tnathtgggg ngtnttygtn 60

gcnggnwsnw sntgyacnga yaaraaycar acnacncara ayaaywsnws nwsnccnytn 120

acncargtna ayacnacngt nwsngtncar athggnacna argcnytnyt ntgytgytty 180

wsnathccny tnacnaargc ngtnytnath acntggatha thaarytnmg nggnytnccn 240

wsntgyacna thgcntayaa rgtngayacn aaracnaayg aracnwsntg yytnggnmgn 300

aayathacnt gggcnwsnac nccngaycay wsnccngary tncarathws ngcngtnacn 360

ytncarcayg arggnacnta yacntgygar acngtnacnc cngarggnaa yttygaraar 420

aaytaygayy tncargtnyt ngtnccnccn gargtnacnt ayttyccnga raaraaymgn 480

wsngcngtnt gygargcnat ggcnggnaar ccngcngcnc arathwsntg gwsnccngay 540

ggngaytgyg tnacnacnws ngarwsncay wsnaayggna cngtnacngt nmgnwsnacn 600

tgycaytggg arcaraayaa ygtnwsngay gtnwsntgya thgtnwsnca yytnacnggn 660

aaycarwsny tnwsnathga rytnwsnmgn ggnggnaayc arwsnytnmg nccntayath 720

ccntayatha thccnwsnat hathathytn athathathg gntgyathtg yytnytnaar 780

athwsnggnt tymgnaartg yaarytnccn aarytngarg cnacnwsngc nathgargar 840

gaygaratgc arccntaygc nwsntayacn garaarwsna ayccnytnta ygayacngtn 900

acnaargtng argcnttycc ngtnwsncar ggngargtna ayggnacnga ytgyytnacn 960

ytnwsngcna thggnath 978

<210> 16
<211> 750
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(750)
<223> N may be a, c, g, or t.

<400> 16
atgggnggna arcaratgac ncaraaytay wsnacnatht tygcngargg naayathwsn 60

carccngtny tnatggayat haaygcngtn ytntgytgyc cnccnathgc nytnmgnaay 120

ytnathatha thacntggga rathathytn mgnggncarc cnwsntgyac naargcntay 180

aaraargara cnaaygarac naargaracn aaytgyacng tngarmgnat hacntgggtn 240

wsnmgnccng aycaraayws ngayytncar athmgnccng tngayacnac ncaygayggn 300

taytaymgng gnathgtngt nacnccngay ggnaayttyc aymgnggnta ycayytncar 360

gtnytngtna cnccngargt naayytntty carwsnmgna ayathacngc ngtntgyaar 420

gcngtnacng gnaarccngc ngcncarath wsntggathc cngarggnws nathytngcn 480

acnaarcarg artaytgggg naayggnacn gtnacngtna arwsnacntg yccntgggar 540

ggncayaarw snacngtnac ntgycaygtn wsncayytna cnggnaayaa rwsnytnwsn 600

gtnaarytna aywsnggnyt nmgnacnwsn ggnwsnccng cnytnwsnyt nytnathath 660

ytntaygtna arytnwsnyt nttygtngtn athytngtna cnacnggntt ygtnttytty 720

carmgnatha aycaygtnmg naargtnytn 750

<210> 17
<211> 582
<212> DNA
<213> rodent

<220>
<221> misc_feature
<222> (1)..(582)
<223> n may be a, c, g, or t.

<400> 17
mgnggncarc cnwsntgyat hatggcntay aargtngara cnaargarac naaygaracn 60

tgyytnggnm gnaayathac ntgggcnwsn acnccngayc ayathccnga yytncarath 120

wsngcngtng cnytncarca ygarggnaay tayytntgyg arathacnac nccngarggn 180

aayttycaya argtntayga yytncargtn ytngtnccnc cngargtnac ntayttyytn 240

ggngaraaym gnacngcngt ntgygargcn atggcnggna arccngcngc ncarathwsn 300

tggacnccng ayggngaytg ygtnacnaar wsngarwsnc aywsnaaygg nacngtnacn 360

gtnmgnwsna cntgycaytg ggarcaraay aaygtnwsng cngtnwsntg yathgtnwsn 420

caywsnacng gnaaycarws nytnwsnath garytnwsnm gnggnacnac nwsnacnacn 480

ccnwsnytny tnacnathyt ntaygtnaar atggtnytny tnggnathat hytnytnaar 540

gtnggnttyg cnttyttyca raarmgnaay gtnacnmgna cn 582

<210> 18
<211> 834
<212> DNA
<213> rodent

<220>
<221> misc_feature
<222> (1)..(834)
<223> n may be a, t, g, or c.

<400> 18
atgcaygcny tnggnmgnac nytngcnytn atgytnytna thttyathac nathytngtn 60

ccngarwsnw sntgywsngt naarggnmgn gargarathc cnccngayga ywsnttyccn 120

ttywsngayg ayaayathtt yccngayggn gtnggngtna cnatggarat hgarathath 180

acnccngtnw sngtncarat hggnathaar gcncarytnt tytgycaycc nwsnccnwsn 240

aargargcna cnytnmgnat htgggarath acnccnmgng aytggccnws ntgymgnytn 300

ccntaymgng cngarytnca rcarathwsn aaraaratht gyacngarmg nggnacnacn 360

mgngtnccng cncaycayca rwsnwsngay ytnccnatha arwsnatggc nytnaarcay 420

gayggncayt aywsntgymg nathgaracn acngayggna thttycarga rmgncaywsn 480

athcargtnc cnggngaraa ymgnacngtn gtntgygarg cnathgcnws naarccngcn 540

atgcarathy tntggacncc ngaygargay tgygtnacna arwsnaarws ncayaaygay 600

acnatgathg tnmgnwsnaa rtgycaymgn garaaraaya ayggncayws ngtnttytgy 660

ttyathwsnc ayytnacnga yaaytggath ytnwsnatgg arcaraaymg nggnacnacn 720

wsnathytnc cnwsnytnyt nwsnathytn taygtnaary tngcngtnac ngtnytnath 780

gtnggnttyg cnttyttyca raarmgnaay tayttymgng tnccngargg nwsn 834

<210> 19
<211> 1047
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1044)
<223>

<400> 19
atg ctc tgc cct tgg aga act gct aac cta ggg cta ctg ttg att ttg 48
Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1 5 10 15

act atc ttc tta gtg gcc gaa gcg gag ggt gct gct caa cca aac aac 96
Thr Ile Phe Leu Val Ala Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn
20 25 30

tca tta atg ctg caa act agc aag gag aat cat gct tta gct tca agc 144
Ser Leu Met Leu Gln Thr Ser Lys Glu Asn His Ala Leu Ala Ser Ser
35 40 45

agt tta tgt atg gat gaa aaa cag att aca cag aac tac tcg aaa gta 192
Ser Leu Cys Met Asp Glu Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val
50 55 60

ctc gca gaa gtt aac act tca tgg cct gta aag atg gct aca aat gct 240
Leu Ala Glu Val Asn Thr Ser Trp Pro Val Lys Met Ala Thr Asn Ala
65 70 75 80

```
gtg ctt tgt tgc cct cct atc gca tta aga aat ttg atc ata ata aca      288
Val Leu Cys Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr
                85                  90                  95

tgg gaa ata atc ctg aga ggc cag cct tcc tgc aca aaa gcc tac agg      336
Trp Glu Ile Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Arg
            100                 105                 110

aaa gaa aca aat gag acc aag gaa acc aac tgt act gat gag aga ata      384
Lys Glu Thr Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile
        115                 120                 125

acc tgg gtc tcc aga cct gat cag aat tcg gac ctt cag att cgt cca      432
Thr Trp Val Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro
    130                 135                 140

gtg gcc atc act cat gac ggg tat tac aga tgc ata atg gta aca cct      480
Val Ala Ile Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro
145                 150                 155                 160

gat ggg aat ttc cat cgt gga tat cac ctc caa gtg tta gtt aca cct      528
Asp Gly Asn Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro
                165                 170                 175

gaa gtg acc ctg ttt caa aac agg aat aga act gca gta tgc aag gca      576
Glu Val Thr Leu Phe Gln Asn Arg Asn Arg Thr Ala Val Cys Lys Ala
            180                 185                 190

gtt gca ggg aag cca gct gcg cag atc tcc tgg atc cca gag ggc gat      624
Val Ala Gly Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Asp
        195                 200                 205

tgt gcc act aag caa gaa tac tgg agc aat ggc aca gtg act gtt aag      672
Cys Ala Thr Lys Gln Glu Tyr Trp Ser Asn Gly Thr Val Thr Val Lys
    210                 215                 220

agt aca tgc cac tgg gag gtc cac aat gtg tct acc gtg acc tgc cac      720
Ser Thr Cys His Trp Glu Val His Asn Val Ser Thr Val Thr Cys His
225                 230                 235                 240

gtc tcc cat ttg act ggc aac aag agt ctg tac ata gag cta ctt cct      768
Val Ser His Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro
                245                 250                 255

gtt cca ggt gcc aaa aaa tca gca aaa tta tat att cca tat atc atc      816
Val Pro Gly Ala Lys Lys Ser Ala Lys Leu Tyr Ile Pro Tyr Ile Ile
            260                 265                 270

ctt act att att att ttg acc atc gtg gga ttc att tgg ttg ttg aaa      864
Leu Thr Ile Ile Ile Leu Thr Ile Val Gly Phe Ile Trp Leu Leu Lys
        275                 280                 285

gtc aat ggc tgc aga aaa tat aaa ttg aat aaa aca gaa tct act cca      912
Val Asn Gly Cys Arg Lys Tyr Lys Leu Asn Lys Thr Glu Ser Thr Pro
    290                 295                 300

gtt gtt gag gag gat gaa atg cag ccc tat gcc agc tac aca gag aag      960
Val Val Glu Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys
305                 310                 315                 320
```

```
aac aat cct ctc tat gat act aca aac aag gtg aag gca tct cag gca     1008
Asn Asn Pro Leu Tyr Asp Thr Thr Asn Lys Val Lys Ala Ser Gln Ala
                325                 330                 335

tta caa agt gaa gtt gac aca gac ctc cat act tta taa                 1047
Leu Gln Ser Glu Val Asp Thr Asp Leu His Thr Leu
            340                 345
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<210> 20
<211> 348
<212> PRT
<213> Homo sapiens

<400> 20

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Met Leu Cys Pro Trp Arg Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu
1               5                   10                  15

Thr Ile Phe Leu Val Ala Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn
            20                  25                  30

Ser Leu Met Leu Gln Thr Ser Lys Glu Asn His Ala Leu Ala Ser Ser
        35                  40                  45

Ser Leu Cys Met Asp Glu Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val
    50                  55                  60

Leu Ala Glu Val Asn Thr Ser Trp Pro Val Lys Met Ala Thr Asn Ala
65                  70                  75                  80

Val Leu Cys Cys Pro Pro Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr
                85                  90                  95

Trp Glu Ile Ile Leu Arg Gly Gln Pro Ser Cys Thr Lys Ala Tyr Arg
            100                 105                 110

Lys Glu Thr Asn Glu Thr Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile
        115                 120                 125

Thr Trp Val Ser Arg Pro Asp Gln Asn Ser Asp Leu Gln Ile Arg Pro
    130                 135                 140

Val Ala Ile Thr His Asp Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro
145                 150                 155                 160

Asp Gly Asn Phe His Arg Gly Tyr His Leu Gln Val Leu Val Thr Pro
                165                 170                 175

Glu Val Thr Leu Phe Gln Asn Arg Asn Arg Thr Ala Val Cys Lys Ala
```

180 185 190

Val Ala Gly Lys Pro Ala Ala Gln Ile Ser Trp Ile Pro Glu Gly Asp
195 200 205

Cys Ala Thr Lys Gln Glu Tyr Trp Ser Asn Gly Thr Val Thr Val Lys
210 215 220

Ser Thr Cys His Trp Glu Val His Asn Val Ser Thr Val Thr Cys His
225 230 235 240

Val Ser His Leu Thr Gly Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro
245 250 255

Val Pro Gly Ala Lys Lys Ser Ala Lys Leu Tyr Ile Pro Tyr Ile Ile
260 265 270

Leu Thr Ile Ile Ile Leu Thr Ile Val Gly Phe Ile Trp Leu Leu Lys
275 280 285

Val Asn Gly Cys Arg Lys Tyr Lys Leu Asn Lys Thr Glu Ser Thr Pro
290 295 300

Val Val Glu Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys
305 310 315 320

Asn Asn Pro Leu Tyr Asp Thr Thr Asn Lys Val Lys Ala Ser Gln Ala
325 330 335

Leu Gln Ser Glu Val Asp Thr Asp Leu His Thr Leu
340 345

<210> 21
<211> 1044
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1044)
<223> n may be a, t, g, or c.

<400> 21
atgytntgyc cntggmgnac ngcnaayytn ggnytnytny tnathytnac nathttyytn 60

gtngcngarg cngarggngc ngcncarccn aayaaywsny tnatgytnca racnwsnaar 120

garaaycayg cnytngcnws nwsnwsnytn tgyatggayg araarcarat hacncaraay 180

```
taywsnaarg tnytngcnga rgtnaayacn wsntggccng tnaaratggc nacnaaygcn    240

gtnytntgyt gyccnccnat hgcnytnmgn aayytnatha thathacntg ggarathath    300

ytnmgnggnc arccnwsntg yacnaargcn taymgnaarg aracnaayga racnaargar    360

acnaaytgya cngaygarmg nathacntgg gtnwsnmgnc cngaycaraa ywsngayytn    420

carathmgnc cngtngcnat hacncaygay ggntaytaym gntgyathat ggtnacnccn    480

gayggnaayt tycaymgngg ntaycayytn cargtnytng tnacnccnga rgtnacnytn    540

ttycaraaym gnaaymgnac ngcngtntgy aargcngtng cnggnaarcc ngcngcncar    600

athwsntgga thccngargg ngaytgygcn acnaarcarg artaytggws naayggnacn    660

gtnacngtna arwsnacntg ycaytgggar gtncayaayg tnwsnacngt nacntgycay    720

gtnwsncayy tnacnggnaa yaarwsnytn tayathgary tnytnccngt nccnggngcn    780

aaraarwsng cnaarytnta yathccntay athathytna cnathathat hytnacnath    840

gtnggnttya thtggytnyt naargtnaay ggntgymgna artayaaryt naayaaracn    900

garwsnacnc cngtngtnga rgargaygar atgcarccnt aygcnwsnta yacngaraar    960

aayaayccny tntaygayac nacnaayaar gtnaargcnw sncargcnyt ncarwsngar   1020

gtngayacng ayytncayac nytn                                          1044
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<210> 22
<211> 813
<212> DNA
<213> rodent

<220>
<221> CDS
<222> (1)..(810)
<223>

<400> 22

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atg cat gct ctg ggg agg att ccg act ttg act ttg ctg atc ttc atc       48
Met His Ala Leu Gly Arg Ile Pro Thr Leu Thr Leu Leu Ile Phe Ile
1               5                  10                  15

aat att ttt gtg tct ggg tca agt tgt act gat gag aat caa aca ata       96
Asn Ile Phe Val Ser Gly Ser Ser Cys Thr Asp Glu Asn Gln Thr Ile
            20                  25                  30

cag aat gac agt tca tct tct ctg aca caa gtt aac act aca atg tct      144
Gln Asn Asp Ser Ser Ser Ser Leu Thr Gln Val Asn Thr Thr Met Ser
        35                  40                  45

gta cag atg gat aaa aag gct ctg ctc tgc tgc ttt tct agt cca ctg      192
Val Gln Met Asp Lys Lys Ala Leu Leu Cys Cys Phe Ser Ser Pro Leu
    50                  55                  60

ata aat gca gta tta atc aca tgg ata ata aaa cac aga cac ctg cct      240
Ile Asn Ala Val Leu Ile Thr Trp Ile Ile Lys His Arg His Leu Pro
```

```
65                  70                  75                  80

tcc tgc aca ata gca tac aac cta gat aaa aag acc aat gaa acc agc      288
Ser Cys Thr Ile Ala Tyr Asn Leu Asp Lys Lys Thr Asn Glu Thr Ser
                85                  90                  95

tgc ttg ggc agg aac atc acc tgg gcc tcc aca cct gac cac agt cct      336
Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro Asp His Ser Pro
            100                 105                 110

gaa ctt cag atc agt gca gtg gcc ctc cag cat gag ggg act tac aca      384
Glu Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Thr Tyr Thr
        115                 120                 125

tgt gag ata gta aca cct gaa ggg aat tta gaa aaa gtc tat gac ctc      432
Cys Glu Ile Val Thr Pro Glu Gly Asn Leu Glu Lys Val Tyr Asp Leu
    130                 135                 140

caa gtg ctg gtg ccc cct gag gta acc tac ttt cca ggg aaa aac aga      480
Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Pro Gly Lys Asn Arg
145                 150                 155                 160

act gca gtc tgt gag gca atg gca ggc aag cct gct gca cag atc tct      528
Thr Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala Ala Gln Ile Ser
                165                 170                 175

tgg act cca gat ggg gac tgt gtc act aag agt gag tca cac agc aat      576
Trp Thr Pro Asp Gly Asp Cys Val Thr Lys Ser Glu Ser His Ser Asn
            180                 185                 190

ggc act gtg act gtc agg agc acg tgc cac tgg gag cag aac aat gtg      624
Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Asn Asn Val
        195                 200                 205

tct gtt gtg tcc tgc tta gtc tct cat tcg act ggt aat cag tct ctg      672
Ser Val Val Ser Cys Leu Val Ser His Ser Thr Gly Asn Gln Ser Leu
    210                 215                 220

tcc ata gaa ctg agt caa ggt aca atg acc acc ccc cgt tcc ttg ctg      720
Ser Ile Glu Leu Ser Gln Gly Thr Met Thr Thr Pro Arg Ser Leu Leu
225                 230                 235                 240

acc att ctc tat gtg aaa atg gcc ctt ttg gtg att att ctt ctt aac      768
Thr Ile Leu Tyr Val Lys Met Ala Leu Leu Val Ile Ile Leu Leu Asn
                245                 250                 255

gta gga ttt gct ttc ttc cag aag aga aat ttt gcc aga aca tga          813
Val Gly Phe Ala Phe Phe Gln Lys Arg Asn Phe Ala Arg Thr
            260                 265                 270
```

<210> 23
<211> 270
<212> PRT
<213> rodent

<400> 23

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Met His Ala Leu Gly Arg Ile Pro Thr Leu Thr Leu Leu Ile Phe Ile
1               5                   10                  15
```

```
Asn Ile Phe Val Ser Gly Ser Ser Cys Thr Asp Glu Asn Gln Thr Ile
            20                  25                  30

Gln Asn Asp Ser Ser Ser Ser Leu Thr Gln Val Asn Thr Thr Met Ser
        35                  40                  45

Val Gln Met Asp Lys Lys Ala Leu Leu Cys Cys Phe Ser Ser Pro Leu
    50                  55                  60

Ile Asn Ala Val Leu Ile Thr Trp Ile Ile Lys His Arg His Leu Pro
65                  70                  75                  80

Ser Cys Thr Ile Ala Tyr Asn Leu Asp Lys Lys Thr Asn Glu Thr Ser
                85                  90                  95

Cys Leu Gly Arg Asn Ile Thr Trp Ala Ser Thr Pro Asp His Ser Pro
            100                 105                 110

Glu Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Thr Tyr Thr
        115                 120                 125

Cys Glu Ile Val Thr Pro Glu Gly Asn Leu Glu Lys Val Tyr Asp Leu
    130                 135                 140

Gln Val Leu Val Pro Pro Glu Val Thr Tyr Phe Pro Gly Lys Asn Arg
145                 150                 155                 160

Thr Ala Val Cys Glu Ala Met Ala Gly Lys Pro Ala Ala Gln Ile Ser
                165                 170                 175

Trp Thr Pro Asp Gly Asp Cys Val Thr Lys Ser Glu Ser His Ser Asn
            180                 185                 190

Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Asn Asn Val
        195                 200                 205

Ser Val Val Ser Cys Leu Val Ser His Ser Thr Gly Asn Gln Ser Leu
    210                 215                 220

Ser Ile Glu Leu Ser Gln Gly Thr Met Thr Thr Pro Arg Ser Leu Leu
225                 230                 235                 240

Thr Ile Leu Tyr Val Lys Met Ala Leu Leu Val Ile Ile Leu Leu Asn
                245                 250                 255
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Val Gly Phe Ala Phe Phe Gln Lys Arg Asn Phe Ala Arg Thr
260 265 270

<210> 24
<211> 810
<212> DNA
<213> rodent

<220>
<221> misc_feature
<222> (1)..(810)
<223> n may be a, t, g, or c.

<400> 24
atgcaygcny tnggnmgnat hccnacnytn acnytnytna thttyathaa yathttygtn 60

wsnggnwsnw sntgyacnga ygaraaycar acnathcara aygaywsnws nwsnwsnytn 120

acncargtna ayacnacnat gwsngtncar atggayaara argcnytnyt ntgytgytty 180

wsnwsnccny tnathaaygc ngtnytnath acntggatha thaarcaymg ncayytnccn 240

wsntgyacna thgcntayaa yytngayaar aaracnaayg aracnwsntg yytnggnmgn 300

aayathacnt gggcnwsnac nccngaycay wsnccngary tncarathws ngcngtngcn 360

ytncarcayg arggnacnta yacntgygar athgtnacnc cngarggnaa yytngaraar 420

gtntaygayy tncargtnyt ngtnccnccn gargtnacnt ayttyccngg naaraaymgn 480

acngcngtnt gygargcnat ggcnggnaar ccngcngcnc arathwsntg gacnccngay 540

ggngaytgyg tnacnaarws ngarwsncay wsnaayggna cngtnacngt nmgnwsnacn 600

tgycaytggg arcaraayaa ygtnwsngtn gtnwsntgyy tngtnwsnca ywsnacnggn 660

aaycarwsny tnwsnathga rytnwsncar ggnacnatga cnacnccnmg nwsnytnytn 720

acnathytnt aygtnaarat ggcnytnytn gtnathathy tnytnaaygt nggnttygcn 780

ttyttycara armgnaaytt ygcnmgnacn 810